

1 AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGACGCAGGAC  
61 ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC  
121 CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC  
1 M D D S T E R E Q S R L  
181 TTA CT TCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCC  
13 T S C L K K R E E M K L K E C V S I L P  
241 CACGGAAGGAAAGCCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT  
33 R K E S P S V R S S K D G K L L A A T L  
301 TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCC  
53 L L A L L S C C L T V V S F Y Q V A A L  
361 TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC  
73 Q G D L A S L R A E L Q G H H A E K L P  
421 CAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC  
93 A G A G A P K A G L E E A P A V T A G L  
481 TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA  
113 K I F E P P A P G E G N S S Q N S R N K  
541 AGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG  
133 R A V Q G P E E T V T Q D C L Q L I A D

FIG.1A

601 ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT  
153 S E T P T I Q K G S Y T F V P W L L S F

661 TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTT  
173 K R G S A L E E K E N K I L V K E T G Y

721 ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA  
193 F F I Y G Q V L Y T D K T Y A M G H L I

781 TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT  
213 Q R K K V H V F G D E L S L V T L F R C

841 GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTACAGCTGGCATTGCAA  
233 I Q N M P E T L P N N S C Y S A G I A K

901 AACTGGAAGAAGGAGATGAACTCCAACCTTGAATACCAAGAGAAAATGCACAAATATCAC  
253 L E E G D E L Q L A I P R E N A Q I S L

961 TGGATGGAGATGTCACATTTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGT  
273 D G D V T F F G A L K L L

1021 CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA

1081 CCAAAAAAAAAAAAAAAAAA

FIG.1B

1	M	S	T	E	S	M	I	-	-	-	-	-	-	-	-	-	-	R	D	V	E	L	TNFA1pha	
1	M	T	P	P	E	R	L	F	L	P	R	V	-	-	-	-	-	-	-	-	-	-	TNFBeta	
1	M	G	A	L	G	L	-	-	-	-	-	-	-	-	-	-	-	E	G	R	G	R	LTbeta	
1	M	Q	Q	P	F	N	Y	P	Y	P	Q	I	Y	W	V	D	S	S	A	S	P	W	A	FASL
1	M	D	D	S	T	E	R	E	Q	S	R	L	-	-	-	-	-	T	S	C	L	K	R	Neutrokine alpha
13	-	A	-	E	E	A	L	P	K	K	T	G	-	-	-	-	-	-	-	-	-	-	-	TNFA1pha
13	-	-	G	G	T	T	L	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFBeta	
14	-	Q	G	R	G	S	L	-	-	-	-	-	-	-	-	-	-	L	L	A	V	A	LTbeta	
31	-	P	C	P	T	S	V	P	R	R	P	G	Q	R	R	P	P	P	P	P	P	P	P	FASL
25	K	E	C	V	S	I	L	P	R	K	-	-	E	S	P	S	V	R	S	S	K	D	G	Neutrokine alpha
23	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	P	Q	G	S	TNFA1pha	
19	-	-	-	-	-	-	-	-	L	L	L	-	-	-	-	-	-	-	L	G	L	L	TNFBeta	
26	A	T	S	L	V	T	-	-	L	L	L	A	-	-	-	-	-	-	-	-	V	P	I	LTbeta
60	P	P	P	L	P	P	-	-	L	P	L	P	P	L	K	K	R	G	N	H	S	T	G	FASL
53	L	L	A	L	L	S	C	C	L	T	V	V	S	F	Y	Q	V	A	A	L	Q	G	D	Neutrokine alpha
36	F	S	F	L	-	-	I	-	-	-	V	A	G	A	T	T	L	F	C	L	L	H	F	TNFA1pha
29	L	P	G	A	Q	G	L	-	-	-	P	G	V	G	L	-	-	-	-	-	-	-	-	TNFBeta
41	L	A	V	L	A	L	V	-	-	-	P	Q	D	Q	G	G	L	-	-	-	-	-	-	LTbeta
88	F	M	V	L	V	A	L	-	-	-	V	G	L	G	L	G	M	F	Q	L	F	H	L	FASL
83	L	Q	G	H	H	A	E	K	L	P	A	G	A	G	A	P	K	A	G	L	E	E	A	Neutrokine alpha

FIG.2A

61	E	-	-	E	S	P	R	D	L	S	L	I	S	P	L	A	Q	A	V	R	S	S	S	R	T	P	S	D	-	-	TNF $\alpha$	
41	-	-	-	-	-	-	-	-	-	-	T	P	S	A	A	Q	T	A	R	Q	H	P	K	M	H	L	A	H	S	T	TNF $\beta$	
59	A	-	-	D	P	G	A	Q	A	Q	Q	G	L	G	F	Q	K	L	P	E	E	E	P	T	D	L	S	P	G	LT $\beta$		
115	R	-	-	E	S	T	S	Q	M	H	T	A	S	S	L	E	K	Q	I	G	H	P	S	P	P	E	K	K	E	FASL		
113	K	I	F	E	P	A	P	G	E	G	N	S	S	Q	N	S	R	N	K	R	A	V	Q	Q	P	E	E	T	V	Neutrokine $\alpha$		
87	-	K	P	V	A	H	V	V	A	N	P	Q	A	E	G	-	Q	-	-	-	-	-	-	-	-	-	-	-	-	TNF $\alpha$		
61	L	K	P	A	A	H	L	I	G	D	P	S	K	Q	N	-	S	-	-	-	-	-	-	-	-	-	-	-	-	TNF $\beta$		
87	L	-	P	A	A	H	L	I	G	A	P	L	K	-	G	Q	G	-	-	-	-	-	-	-	-	-	-	-	-	LT $\beta$		
143	L	R	K	V	A	H	L	T	G	K	S	N	S	R	S	M	P	-	-	-	-	-	-	-	-	-	-	-	-	FASL		
143	T	Q	D	C	L	Q	L	I	A	D	S	E	T	P	T	I	Q	K	G	S	Y	T	F	V	P	W	L	-	-	-	Neutrokine $\alpha$	
109	A	N	A	L	L	A	N	G	V	E	L	R	D	N	-	Q	L	V	V	P	S	E	G	L	Y	L	I	Y	S	Q	TNF $\alpha$	
84	D	R	A	F	L	Q	D	G	F	S	L	S	N	N	-	S	L	L	V	P	T	S	G	I	Y	F	V	Y	S	Q	TNF $\beta$	
109	E	Q	A	F	L	T	S	G	T	Q	F	S	D	A	E	G	L	A	L	P	Q	D	G	L	Y	Y	C	L	-	-	LT $\beta$	
167	G	I	V	L	L	-	S	G	V	K	Y	K	K	G	-	G	L	V	I	N	E	T	G	L	Y	F	V	Y	S	K	FASL	
170	-	L	S	F	K	R	G	S	A	L	E	E	K	E	N	K	I	L	V	K	E	T	G	Y	F	F	I	Y	G	Q	Neutrokine $\alpha$	
138	V	L	F	K	G	Q	G	C	-	-	-	-	-	-	-	P	S	T	H	V	L	L	T	H	T	I	S	R	I	A	V	TNF $\alpha$
113	V	V	F	S	G	K	A	Y	-	-	S	P	K	A	P	S	S	P	L	Y	L	A	H	E	V	Q	L	F	S	S	TNF $\beta$	
139	V	G	Y	R	G	R	A	P	P	G	G	G	D	P	Q	G	R	S	V	T	L	R	S	S	L	Y	R	A	G	G	LT $\beta$	
195	V	Y	F	R	G	Q	S	C	-	-	N	-	-	-	-	-	N	L	P	L	S	H	K	V	Y	M	R	N	S	-	FASL	
199	V	L	Y	T	D	K	T	Y	A	M	G	-	-	-	-	-	-	H	L	I	Q	R	K	K	V	H	V	F	G	D	Neutrokine $\alpha$	

FIG.2B

162	S	Y	Q	T	K	V	N	-	-	L	L	S	A	I	K	S	P	C	Q	R	E	T	P	E	-	-	G	A	E	A	TNFalpha	
141	Q	Y	P	F	H	V	P	-	-	L	L	S	S	Q	K	M	V	Y	P	-	-	-	-	-	-	-	G	L	Q		TNFbeta	
169	A	Y	G	P	G	T	P	E	L	L	L	E	G	A	E	T	V	T	P	V	L	D	P	A	R	R	Q	Y	G		LTbeta	
217	K	Y	P	Q	D	L	V	-	-	M	M	E	G	K	M	M	S	Y	C	-	-	-	-	-	-	-	T	T	G		FASL	
223	E	L	S	-	-	L	V	T	L	F	R	C	I	Q	N	M	P	E	T	L	P	N	-	-	-	-	-	-	-	-		Neutrokin alpha
188	K	P	W	Y	E	P	I	Y	L	G	G	V	F	Q	L	E	K	G	D	R	L	S	A	E	I	N	R	P	D	Y	TNFalpha	
161	E	P	W	L	H	S	M	Y	H	G	A	A	F	Q	L	T	Q	G	D	Q	L	S	T	H	T	D	G	I	P	H		TNFbeta
199	P	L	W	Y	T	S	V	G	F	G	L	V	Q	L	R	R	G	E	R	V	Y	V	N	I	S	H	P	D	M			LTbeta
237	Q	M	W	A	R	S	S	Y	L	G	A	V	F	N	L	T	S	A	D	H	L	Y	V	N	V	S	E	L	S	L		FASL
243	-	-	-	-	N	S	C	Y	S	A	G	I	A	K	L	E	E	G	D	E	L	Q	L	A	I	P	R	E	N	A		Neutrokin alpha
218	L	D	F	A	E	S	G	Q	V	Y	F	G	I	I	A	L																TNFalpha
191	L	V	L	S	P	S	-	T	V	F	F	G	A	F	A	L																TNFbeta
229	V	D	F	A	R	-	G	K	T	F	F	G	A	V	M	V	G															LTbeta
267	V	N	F	E	S	-	Q	T	F	F	G	L	Y	K	L																	FASL
269	Q	I	S	L	D	G	D	V	T	F	F	G	A	L	K	L	L															Neutrokin alpha

FIG.2C

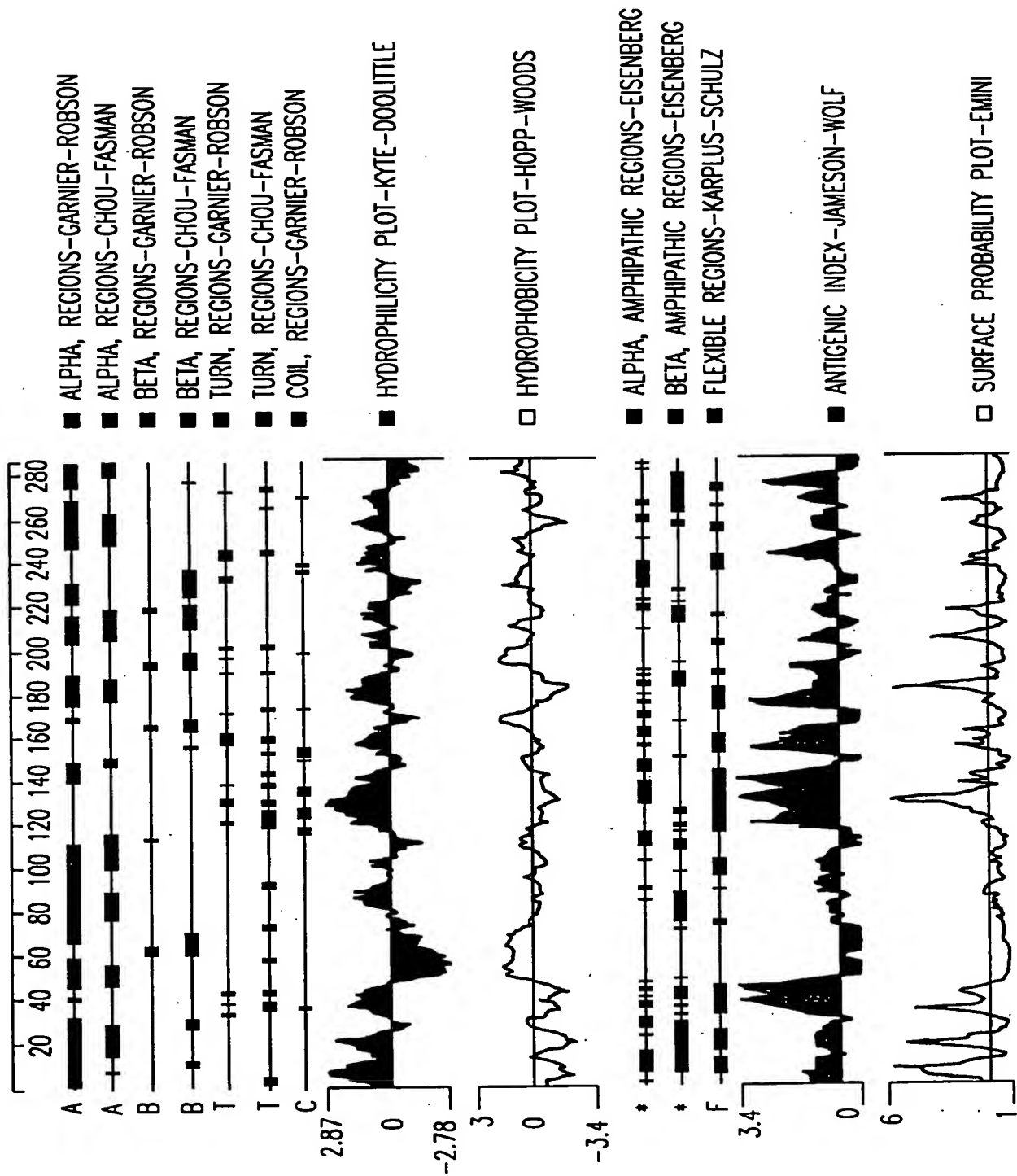


FIG.3

	1				50
HSOAD55R	.....A	GGNTAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HNEDU15X	...AAATTCA	GGATAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HSLAH84R	.AATTCGGCA	NAGNAACTG	GTTACTTTT	TATATATGGT	CAGGTTTTAT
HLTBM08R	AATTCGGCAC	GAGCAAGGCC	GGCCTGGAGG	AAGCTCCAGC	TGTCACCGCG
	51				100
HSOAD55R	GTGCACGCAG	GACATCANCA	A..ACACANN	NNNCAGGAAA	TAATCCATTC
HNEDU15X	GTGCACGCAG	GACATCAACA	A..ACACAGA	TAACAGGAAA	TGATCCATTC
HSLAH84R	ATACTGATAA	GACCTACGCC	ATGGGACATC	TAGTTCAGAG	GAAGAAGGTC
HLTBM08R	GGACTGAAAA	TCTTTGAACC	ACCAGCTCCA	GGAGAAGGCA	ACTCCAGTCA
	101				150
HSOAD55R	CCTGTGGTCA	CTTATTCTAA	AGGCCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HNEDU15X	CCTGTGGTCA	CTTATTCTAA	AGGCCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HSLAH84R	CATGCTTTTG	GGGATGAATT	GAGTCTGGTG	ACTTTGTTTC	GATGTATTCA
HLTBM08R	GAACAGCAGA	AATAAGCGTG	CCGTTCAGGG	TCCAGAAGAA	ACAGTCACTC
	151				200
HSOAD55R	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HNEDU15X	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HSLAH84R	AAATATGCCT	GAAACACTAC	CCAATAATTC	CTGCTATTCA	GCTGGCATTG
HLTBM08R	AAGACTGCTT	GCAACTGNTT	GCAGACAGTG	AAACACCAAC	TATACAAAAA
	201				250
HSOAD55R	AGAAAAGAGA	AGAAATGAAA	CTGNAAGGAG	TGTGTTTCCA	TCCTCCCACG
HNEDU15X	AGAAAAGAGA	AGAAATGAAA	CT.GAAGGAG	TGTGTTTCCA	TCCTCCCACG
HSLAH84R	CAAAACTGGN	AGGAAGGA..	...GATGAAC	TCCAAC TTGC	AATACCAGGG
HLTBM08R	GGCTCCCTTC	TGNTGCCACA	TTTGGGCCAA	GGAATGGAGA	GATTTCTTCG
	251				300
HSOAD55R	GAAGGAAAGC	CCCTCTNTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HNEDU15X	GAAGGAAAGC	CCCTCTGTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HSLAH84R	GAAAATGCAC	AATTATCACT	GGGATGGAGA	TGTTACATT	TTTTGGGTGC
HLTBM08R	TCTGGAAACA	TTTTGCCAAA	CTCTTCAGAT	ACTCTTNCT	CTCTGGGAAT
	301				350
HSOAD55R	CAACCTTGNT	GNTGGCATTG	TGTTCTTGCT	GNCTCAAGGT	GGTGTTNTT.
HNEDU15X	CAACCTTGCT	GCTGGCACTG	CTGTCTTGCT	GCCTCACGGT	GGTGTCTTTC
HSLAH84R	CATTGAAACT	GCTGTGACCT	NCTTACANCA	NGTGCTGTTN	GCTATTTTNC
HLTBM08R	CAAAGGAAAA	TCTCTACTTA	GATTNACACA	TTTGTTCCCA	TGGGTNTCTT
	351				400
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	TACCAGGTGG	CCGCCCTGCA	AGGGGACCTG	GCCAGCCTCC	GGGCAGAGCT
HSLAH84R	CTNCCTNTTC	TNTGGTAACC	TCTTAGGAAG	GAAGGATTCT	TAAGTGGGAA
HLTBM08R	AAGTTTTAAA	AGGGGAGTGC	CCTTAGGAGG	AAAAGGGGAT	AAATATTGGC

FIG.4A

	401		450
HSOAD55R	.....	.....	.....
HNEDU15X	GCAGGGCCAC	CACGCGGAGA	AGCTGCCAGC
HSLAH84R	ATAACCCAAA	AAAANNTTAA	ANGGGTANGN
HLTBM08R	CAAGGNACTG	GTTANTTTNT	AAATATGGTC
		AGGTTTNTAT	ANCTGGTAGG
	451		500
HSOAD55R	.....	.....	.....
HNEDU15X	CCGGCCTGGA	GGAAGCTCCA	GCTGTCACCG
HSLAH84R	CNNGNNGNNT	TTTNGGNNTA	TNTTNTNNTN
HLTBM08R	CCTCGCCATG	GGCATTNATT	CANGGNGAGG
		NCNNTCTTTT	GGGNTGA...
	501		550
HSOAD55R	.....	.....	.....
HNEDU15X	CCACCAGCTC	CAGGAGAAGG	CAACTCCAGT
HSLAH84R	CNANGGGGGN	TTTTT.....	.....
HLTBM08R	.....	.....	.....
	551		600
HSOAD55R	.....	.....	.....
HNEDU15X	TGCCGTTTCA	GGTCCAGAAG	AAACAGTCAC
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	601		650
HSOAD55R	.....	.....	.....
HNEDU15X	TTGCAGACAG	TGAAACACCA	ACTATACAAA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	651		700
HSOAD55R	.....	.....	.....
HNEDU15X	CCATGGCTTC	TCAGCTTTAA	AAGGGGAAGT
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	701		750
HSOAD55R	.....	.....	.....
HNEDU15X	TAAAATATTG	GTCAAAGAAA	CTGGTTACTT
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	751		800
HSOAD55R	.....	.....	.....
HNEDU15X	TATATACTGA	TAAGACCTAC	GCCATGGGAC
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....

FIG.4B



	801		850
HSOAD55R	.....	.....	.....
HNEDU15X	GTCCATGTCT	TTGGGGATGA	ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	851		900
HSOAD55R	.....	.....	.....
HNEDU15X	TCAAAATATG	CCTGAAACAC	TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	901		950
HSOAD55R	.....	.....	.....
HNEDU15X	TTGCAAACT	GGAAGAAGGA	GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	951		1000
HSOAD55R	.....	.....	.....
HNEDU15X	AATGCACAAA	TATCACTGGA	TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	1001		1050
HSOAD55R	.....	.....	.....
HNEDU15X	ACTGCTGTGA	CCTACTTACA	CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	1051		1100
HSOAD55R	.....	.....	.....
HNEDU15X	CTGTACCTCT	AAGAAGAAAG	AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	1101		
HSOAD55R	.....		
HNEDU15X	AAAAAA		
HSLAH84R	.....		
HLTBM08R	.....		

FIG.4C